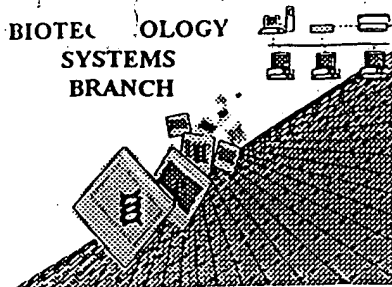


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



TECH CENTER 1600/2900

SEP 07 2001

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/218,913C

Source: 1652

Date Processed by STIC: 7/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1652

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/218,913C

DATE: 07/20/2001

TIME: 13:25:21

Input Set : A:\98,736.SEQ.LST.txt

Output Set: N:\CRF3\07202001\I218913C.raw

3 <110> APPLICANT: Hall, Roderick L
 4 Poll, Christopher T.
 5 Newton, Benjamin B.
 6 Taylor, William J.A.
 8 <120> TITLE OF INVENTION: A Method for Accelerating the Rate of Mucociliary Clearance
 W--> 9 <130> FILE REFERENCE: 98,736
 11 <140> CURRENT APPLICATION NUMBER: 09/218,913C
 12 <141> CURRENT FILING DATE: 1998-12-22
 14 <160> NUMBER OF SEQ ID NOS: 71
 16 <170> SOFTWARE: Microsoft Word 97

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

332 <210> SEQ ID NO: 11
 333 <211> LENGTH: 170
 334 <212> TYPE: PRT
 335 <213> ORGANISM: Homo sapien
 337 <220> FEATURE:
 338 <221> NAME/KEY: peptide
 339 <222> LOCATION: 1..170
 340 <223> OTHER INFORMATION: /note= "Xaa at positions 8, 17, 21-26, 40, 42, 45-47, 52,
 64,
 341 103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any
 342 amino acid residue"
 344 <400> SEQUENCE: 11
 W--> 345 Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val
 346 1 5 10 15
 W--> 348 Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
 349 20 25 30
 W--> 351 Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser
 352 35 40 45
 W--> 354 Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Xaa
 355 50 55 60
 357 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
 358 65 70 75 80
 360 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
 361 85 90 95
 W--> 363 Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys Thr Ala Asn Ala Val Xaa
 364 100 105 110
 W--> 366 Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Tyr Phe Asp Val Glu Arg
 367 115 120 125
 W--> 369 Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Lys Asn
 370 130 135 140
 W--> 372 Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Xaa Gln
 373 145 150 155 160
 375 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
 376 165 170 175

Length shemas 170 but
actual length is 179 (see next
page)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/218,913C

DATE: 07/20/2001
TIME: 13:25:21

Input Set : A:\98,736.SEQ.LST.txt
Output Set: N:\CRF3\07202001\I218913C.raw

E--> 378 Ala Val Ser ⁻¹⁷⁹
537 <210> SEQ ID NO: 16
538 <211> LENGTH: 428 — Length Listed as 428, actual
539 <212> TYPE: DNA length is 431
540 <213> ORGANISM: Homo sapien
542 <220> FEATURE:
543 <221> NAME/KEY: misc_feature
544 <222> LOCATION: 1..430
545 <223> OTHER INFORMATION: /note= "n at positions 3, 11, 12, 17, 51 and 429 represent
any nucleic acid"
547 <400> SEQUENCE: 16

W--> 548 gcngcgcgtt nntcgcntgc tgggatcgct gctgcacctc tctgggggtcg nggcggccga 60
550 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc 120
552 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg 180
554 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc 240
556 cactgtcaca gagaatgccg cgggtgacct ggccaccagc aggaatgcag cggattcctc 300
558 tgtcccaagt gctcccagaa ggcaggattc ttgaagacca cttcagcgat atgttcaact 360
560 atgaagaata ctggcaccgc caacgcattc actgggcctg cgtgcatact tcccacgctg 420
E--> 562 gtactttgnc g 431

893 <210> SEQ ID NO: 35
894 <211> LENGTH: 36 — Length differs
895 <212> TYPE: DNA
896 <213> ORGANISM: Homo sapien
898 <400> SEQUENCE: 35

E--> 899 ggtctagagg ccgggtcggtt tctcgcctgg ctggga 37
1396 <210> SEQ ID NO: 54
1397 <211> LENGTH: 23
1398 <212> TYPE: DNA
1399 <213> ORGANISM: Homo sapien
1401 <220> FEATURE:
1402 <223> OTHER INFORMATION: Human Bikunin protein fragment
1404 <400> SEQUENCE: 54
1405 Met Leu Arg Ala Glu Ala Asp Gly Asn Ser Arg Leu Leu Gly Ser Leu
1406 1 5 10 15
1408 Leu Leu Ser Gly Val Leu Ala
E--> 1409 20
1515 <210> SEQ ID NO: 64
1516 <211> LENGTH: 20 — Length differs
1517 <212> TYPE: PRT
1518 <213> ORGANISM: Homo sapien
1520 <220> FEATURE:
1521 <223> OTHER INFORMATION: /note= "Human Bikunin protein fragment"
1523 <400> SEQUENCE: 64
1524 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1525 1 5 10 15
1527 Val Gly Arg Cys ⁻²¹
E--> 1528 20
1668 <210> SEQ ID NO: 71
1669 <211> LENGTH: 225
1670 <212> TYPE: PRT

RAW SEQUENCE LISTING

DATE: 07/20/2001

PATENT APPLICATION: US/09/218,913C

TIME: 13:25:21

Input Set : A:\98,736.SEQ.LST.txt

Output Set: N:\CRF3\07202001\I218913C.raw

1671 <213> ORGANISM: Homo sapien
1673 <220> FEATURE:
1674 <223> OTHER INFORMATION: /note= "Human Bikunin protein fragment"
1676 <400> SEQUENCE: 71
1677 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
1678 1 5 10 15
1680 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
1681 20 25 30
1683 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
1684 35 40 45
1686 Asn Asn Tyr Leu Thr Lys Glu Cys Leu Lys Lys Cys Ala Thr Val
1687 50 55 60
1689 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
1690 65 70 75 80
1692 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
1693 85 90 95
1695 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
1696 100 105 110
1698 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
1699 115 120 125
1701 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
1702 130 135 140
1704 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
1705 145 150 155 160
1707 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
1708 165 170 175
1710 Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
1711 180 185 190
1713 Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
1714 195 200 205
1716 Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val
1717 210 215 220
1719 Leu
1720 225
E--> 1725 1

remove miscellaneous material at
the end of file

VERIFICATION SUMMARY

DATE: 07/20/2001

PATENT APPLICATION: US/09/218,913C

TIME: 13:25:22

Input Set : A:\98,736.SEQ.LST.txt

Output Set: N:\CRF3\07202001\I218913C.raw

L:9 M:283 W: Missing Blank Line separator, <130> field identifier
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:378 M:252 E: No. of Seq. differs, <211>LENGTH:Input:170 Found:179 SEQ:11
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:426 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:562 M:252 E: No. of Seq. differs, <211>LENGTH:Input:428 Found:431 SEQ:16
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:597 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:899 M:254 E: No. of Bases conflict, LENGTH:Input:37 Counted:36 SEQ:35
L:991 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:1098 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:1205 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:1409 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:0 SEQ:54
L:1528 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:64
L:1725 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:71